

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:35 ; Search time 2351.15 Seconds
(without alignments)
175.416 Million cell updates/sec

Title: US-09-851-670-4

Perfect score: 25

Sequence: 1 acagtagcagcacacagcatgagacc 25

Scoring table: IDENTITY-NUC

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
20: em_or: *
21: em_ov: *
22: em_pat: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_sy: *
28: em_un: *
29: em_vi: *
30: em_htgo_hum: *
31: em_htgo_inv: *
32: em_htgo_rnd: *
33: em_htg_hum: *
34: em_htg_inv: *
35: em_htg_rnd: *
36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	17.6	70.4	38	6	AX054682	AX054682 Sequence
C 2	16.6	66.4	52	12	SYNAPPH	M3498 Synthetic E
C 3	16.2	64.8	36	6	A62704	A62704 Sequence 5
C 4	16.2	64.0	54	6	A62703	A62703 Sequence 4
C 5	16	64.0	51	6	AX164869	AX164869 Sequence
C 6	15.8	63.2	52	6	AR124697	AR124697 Sequence
C 7	15.6	62.4	24	6	AX146991	AX146991 Sequence
C 8	15.6	62.4	39	6	A91016	A91016 Sequence 13
C 9	15.6	62.4	39	6	E50982	E50982 Assay, rece
C 10	15.6	62.4	43	6	AR059527	AR059527 Sequence
C 11	15.6	62.4	50	6	S53635	S53635 Apoa-IV (Ap
C 12	15.4	61.6	60	6	AX190222	AX190222 Sequence
C 13	15.4	61.6	51	6	AX190223	AX190223 Sequence
C 14	15.4	61.6	57	3	AF320169	AF320169 Drosophila
C 15	15.4	61.6	57	3	AF320170	AF320170 Drosophila
C 16	15.4	61.6	57	3	AF320171	AF320171 Drosophila
C 17	15.4	61.6	57	3	AF320172	AF320172 Drosophila
C 18	15.4	61.6	57	3	AF320173	AF320173 Drosophila
C 19	15.4	61.6	57	3	AF320174	AF320174 Drosophila
C 20	15.4	61.6	57	3	AF320175	AF320175 Drosophila
C 21	15.4	61.6	57	3	AF320176	AF320176 Drosophila
C 22	15.4	61.6	57	3	AF320177	AF320177 Drosophila
C 23	15.4	61.6	57	3	AF320178	AF320178 Drosophila
C 24	15.4	61.6	57	3	AF320179	AF320179 Drosophila
C 25	15.4	61.6	60	3	AF320167	AF320167 Drosophila
C 26	15.4	61.6	60	3	AF320168	AF320168 Drosophila
C 27	15.4	61.6	60	3	AF320180	AF320180 Drosophila
C 28	15.2	60.8	26	6	A27957	A27957 Human TCR V
C 29	15.2	60.8	26	6	A31628	A31628 Synthetic h
C 30	15	60.0	40	6	AR059117	AR059117 Sequence
C 31	14.6	58.4	21	6	AR084539	AR084539 Sequence
C 32	14.6	58.4	21	6	AR084571	AR084571 Sequence
C 33	14.6	58.4	21	6	AX104588	AX104588 Sequence
C 34	14.6	58.4	24	6	AR084605	AR084605 Sequence
C 35	14.6	58.4	30	6	AR084541	AR084541 Sequence
C 36	14.6	58.4	30	6	E34522	E34522 SCA7 gene a
C 37	14.6	58.4	30	6	184405	184405 Sequence 6
C 38	14.6	58.4	30	6	184410	184410 Sequence 11
C 39	14.6	58.4	31	6	AR078304	AR078304 Sequence
C 40	14.6	58.4	33	6	AR084540	AR084540 Sequence
C 41	14.6	58.4	36	6	AR084542	AR084542 Sequence
C 42	14.6	58.4	40	6	AR091379	AR091379 Sequence
C 43	14.6	58.4	42	6	A62705	A62705 Sequence 6
C 44	14.6	58.4	44	6	AX090408	AX090408 Sequence
C 45	14.6	58.4	44	6	AX090409	AX090409 Sequence

ALIGNMENTS

RESULT 1
AX054682/c
LOCUS AX054682
DEFINITION Sequence 14 from Patent WO0073788.
ACCESSION AX054682
VERSION AX054682.1 GI:12228208
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 38)
Ng, G. and O'Neill, G.
TITLE
Use of gabapentin in assays to identify gabab receptor modulators
JOURNAL
Patent: WO 0073788-A 14 07-DEC-2000;
Metrick Frost Canada & Co. (CA)
LOCATION/Qualifiers
1..38
source

/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 4 a 11 c 12 g 11 t
ORIGIN

Query Match 70.4%; Score 17.6; DB 6; Length 38;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 caatagacagcaacagcatgacc 25
111111111111111111111111
Db 32 CACGACGACGACGACGATGCTACC 9

RESULT 2
LOCUS SYNALKPH 52 bp DNA SYN 27-APR-1993
DEFINITION Synthetic E.coli alkaline phosphatase gene, partial cds.
ACCESSION M34498
VERSION M34498.1 GI:207911
KEYWORDS alkaline phosphatase.
SOURCE E.coli (strain AM1043) DNA.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 52)
AUTHORS Chou,M.M. and Kendall,D.A.
TITLE Polymeric sequences reveal a functional interrelationship between hydrophobicity and length of signal peptides
JOURNAL J. Biol. Chem. 265, 2873-2880 (1990)
MEDLINE 90153918

FEATURES
source Location/Qualifiers

1..52
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>52
/note="synthetic alkaline phosphatase precursor signal peptide"
CDS
<1..>52
/note="synthetic alkaline phosphatase precursor"
/codon_start=1
/transl_table=11
/protein_id="AA072836.1"
/db_xref="GI:554532"
/translation="STLLLLLLLLTPVTK"

BASE COUNT 9 a 15 c 10 g 18 t
ORIGIN

Query Match 66.4%; Score 16.6; DB 12; Length 52;
Best Local Similarity 82.6%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 acatagacagcaacagcatgag 23
111111111111111111111111
Db 34 ACAGTACAGCAGCAGCAGCAGA 12

RESULT 3
LOCUS A62704 36 bp DNA PAT 12-MAR-1998
DEFINITION Sequence 5 from Patent WO9717445.
ACCESSION A62704
VERSION A62704.1 GI:3716588
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 36)
AUTHORS Tori,L., Lutz,Y., Trotter,Y., Mandel and Jean-Louis.
TITLE METHOD FOR TREATING NEURODEGENERATIVE DISEASES USING A 1c2 ANTIBODY OR A FRAGMENT OR DERIVATIVE THEREOF, AND CORRESPONDING PHARMACEUTICAL COMPOSITIONS
JOURNAL Patent: WO 9717445-A 5 15-MAY-1997;
CENTRE NAT RECH SCIENT (FR)

COMMENT Other publication FR 2741088 19970516.
FEATURES Location/Qualifiers
source 1..36
/organism="unclassified"
/db_xref="taxon:32644"
/clone="DAN26"

BASE COUNT 13 a 12 c 11 g 0 t
ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 36;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 caatagacagcaacagcatgag 22
111111111111111111111111
Db 10 CACGACGACGACGACGACGAG 30

RESULT 4
LOCUS A62703 54 bp DNA PAT 12-MAR-1998
DEFINITION Sequence 4 from Patent WO9717445.
ACCESSION A62703
VERSION A62703.1 GI:3716587
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 54)
AUTHORS Tori,L., Lutz,Y., Trotter,Y., Mandel and Jean-Louis.
TITLE METHOD FOR TREATING NEURODEGENERATIVE DISEASES USING A 1c2 ANTIBODY OR A FRAGMENT OR DERIVATIVE THEREOF, AND CORRESPONDING PHARMACEUTICAL COMPOSITIONS
JOURNAL Patent: WO 9717445-A 4 15-MAY-1997;
CENTRE NAT RECH SCIENT (FR)
OTHER Publication FR 2741088 19970516.
COMMENT Location/Qualifiers

FEATURES
source 1..54
/organism="unclassified"
/db_xref="taxon:32644"
/clone="DAN15"

BASE COUNT 21 a 18 c 15 g 0 t
ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 54;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 caatagacagcaacagcatgag 22
111111111111111111111111
Db 13 CACGACGACGACGACGACGAG 33

RESULT 5
LOCUS AX164869 51 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 64 from Patent WO0138586.
ACCESSION AX164869
VERSION AX164869.1 GI:14545698
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 64 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers

source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism"
Accession number CG43336163"
BASE COUNT 5 a 13 c 20 g 13 t
ORIGIN

Query Match 64.0%; Score 16; DB 6; Length 51;
Best Local Similarity 79.2%; Pred. No. 3.7e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 cagtagcagcaacagcatgagacc 25
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Db 29 CAGTAGCAGCAGCAGCAGCATTCG 6

RESULT 6
ARI24697/c ARI24697 52 bp DNA PAT 16-MAY-2001
LOCUS Sequence 3 from patent US 6172076.
ACCESSION ARI24697
VERSION ARI24697.1 GI:14110058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Emptrey,M.W., Mai,J.S., Perlow,D.S. and Hoffman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6172076-A 3 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..52
BASE COUNT 5 a 15 c 19 g 13 t
ORIGIN

Query Match 63.2%; Score 15.8; DB 6; Length 52;
Best Local Similarity 89.5%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cagtagcagcaacagcatg 20
|||||
Db 43 CAGCAGCAGCAGCAGCATG 25

RESULT 7
AX146991/c AX146991 24 bp DNA PAT 08-JUN-2001
LOCUS Sequence 16 from Patent WO0136610.
ACCESSION AX146991
VERSION AX146991.1 GI:14346262
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Deleenslinder,M., Wieggers,R. and Weske,M.
TITLE Human enzymes of the metalloprotease family
JOURNAL Patent: WO 0136610-A 16 25-MAY-2001;
Solvay Pharmaceuticals B.V. (NL)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Degenerated Forward Primer"

BASE COUNT 1 a 5 c 4 g 7 t 7 others
ORIGIN

Query Match 62.4%; Score 15.6; DB 6; Length 24;
Best Local Similarity 62.5%; Pred. No. 5.5e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 cagtagcagcaacagcatgagacc 25
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Db 24 SAGSAGSAGSAGSAGCATSAGNCC 1

RESULT 8
A91016/c A91016 39 bp DNA PAT 22-JAN-2000
LOCUS Sequence 13 from Patent EP0854185.
ACCESSION A91016
VERSION A91016.1 GI:6739635
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Stacker,S.A. and Wilks,A.F.
TITLE Assay receptor proteins and ligands
JOURNAL Patent: EP 0854185-A 13 22-JUL-1998;
LUDWIG INST CANCER RES (US)
FEATURES Location/Qualifiers
source 1..39
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 7 a 10 c 7 g 15 t
ORIGIN

Query Match 62.4%; Score 15.6; DB 6; Length 39;
Best Local Similarity 81.8%; Pred. No. 5.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 acagtagcagcaacagcatgag 22
|||||
Db 23 ACAGTAGCAGCAGCAGCATCAG 2

RESULT 9
E50982/c E50982 39 bp DNA PAT 07-FEB-2001
LOCUS Assay, receptor protein NYK and ligand.
ACCESSION E50982
VERSION E50982.1 GI:13023215
KEYWORDS JP 2000046833-A/7.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Stacker,S.A.W.M. and Frederic.
TITLE Assay, receptor protein NYK and ligand
JOURNAL Patent: JP 2000046833-A 7 18-FEB-2000;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT OS Artificial Sequence
PN JP 2000046833-A/7
PD 18-FEB-2000
PF 12-APR-1999 JP 1999103424
PR 23-DEC-1994 AU PN 0301.23-DEC-1994 AU PN 0300 PI
STACKER STEVEN ALEN WILKS ANDREW FREDERIC
PC G01N33/566,A61K38/00,A61K39/39,C07K14/52,C07K14/715,
PC C12N5/10,
PC C12N15/02,C12N15/09,C12P21/02,C12P21/08,G01N33/50,
PC G01N33/531,
PC G01N33/543//C12P21/02,C12R1:91,A61K37/02,A61K37/54,C12N5/00,
PC C12N15/00,
PC C12N15/00

CC Key Location/Qualifiers
FH 1..39
FT source /organism="Artificial Sequence".

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ORIGIN	/product="bicoid" /protein_id="AAK38621.1" /db_xref="GI:13752327" /translation="AQFFQTTQDQDQLHQDQDQDQ"				
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Best Local Similarity	94.1%;	Pred. No. 7.3e+03;			
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
OY	2	cagtagcagcagaacgca	18		
Db	40	CAGCAGCAGCAACAGCA	56		
RESULT 15					
LOCUS	AF320170	57 bp	DNA	INV	23-Apr-2001
DEFINITION	Drosophila pseudoobscura strain Mather17 bicoid (bcd) gene, partial cds.				
ACCESSION	AF320170				
VERSION	AF320170.1	GI:13752328			
KEYWORDS	Drosophila pseudoobscura.				
SOURCE	Drosophila pseudoobscura				
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	Noor,M.A., Kliman,R.M. and Machado,C.A.				
AUTHORS	1 (bases 1 to 57)				
TITLE	Evolutionary history of microsatellites in the obscure group of Drosophila				
JOURNAL	Mol. Biol. Evol. 18 (4), 551-556 (2001)				
MEDLINE	21165327				
PUBMED	11264406				
REFERENCE	2 (bases 1 to 57)				
AUTHORS	Noor,M.A.F., Kliman,R.M. and Machado,C.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-NOV-2000) Genetics, Rutgers University, 604 Allison Rd., Piscataway, NJ 08854, USA				
FEATURES	Location/Qualifiers				
source	1..57				
gene	/organism="Drosophila pseudoobscura"				
exon	/strain="Mather17"				
repeat_region	/db_xref="taxon:7237"				
CDS	<1..>57				
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	<1..>57				
	/gene="bcd"				
	/number=3				
	1..57				
	/note="microsatellite"				
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	/gene="bcd"				
	/codon_start=1				
	/product="bicoid"				
	/protein_id="AAK38622.1"				
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	/translation="AQFFQTTQDQDQLHQDQDQDQ"				
BASE COUNT	19 a	19 c	12 g	7 t	
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Best Local Similarity	94.1%;	Pred. No. 7.3e+03;			
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
OY	2	cagtagcagcagaacgca	18		
Db	40	CAGCAGCAGCAACAGCA	56		

Mon Mar 11 07:46:51 2002

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Search completed: March 9, 2002, 00:48:36
Job time: 11117 sec
